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## REMARKS

Applicants respectfully request reconsideration of the present application.

1. Disposition of the Claims and Specification

Claims 44-51, 54, and 58-61 are pending. Claims 44, 50 and 51 are currently amended. Claims 61 and 62 are newly added. Support for the amendment to claim 44 may be found in the specification at page 16, line 31 – page 17, line 2. Support for the amendment to claim 51 may be found in the specification at page 17, lines 8-15. Support for claims 61 and 62 may be found in the specification at page 27, lines 17-18. Claim 50 was dependent on a cancelled claim, as a result of a typographical error, and is amended to be dependent on a pending claim.

Because the foregoing amendments do not introduce new matter, entry thereof by the Examiner is respectfully requested.

2. Specification/Information Disclosure Statement

The Examiner indicates that the documents supplied on 1/20/2004 were not considered because they did not comply with 37 C.F.R. § 1.98. Applicants resubmit these documents in the attached information disclosure statement in conformance with 37 C.F.R. 1.98.

3. Claim Rejections – 35 U.S.C. § 101

Claims 44-51, 54, and 58-59 are rejected under 35 U.S.C. § 101 because the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility. The Examiner reasons that “until some actual and specific significance can be attributed to the protein identified in the specification … the instant invention is incomplete.” Office Action at 3. The Examiner admits that Applicants will satisfy the utility requirement of 35 U.S.C. § 101 by identifying one substantial credible utility, such as an “indicator of a diseased state or of the presence of a disorder.” Office Action at 6. Applicants respectfully request reconsideration and withdrawal of the rejection.

According to the results of the attached BLAST search, performed with SEQ ID NO: 3 of the instant invention, the protein identified in the specification having an amino acid sequence corresponding to SEQ ID NO: 3 is identical to the proteins named p34SEI1 and TRIP-Br1. See BLAST Search Results (Exhibit 1). Sugimoto *et al.*, GENES & DEVELOPMENT 13:3027-3033 (1999), a post-filing date article regarding the p34SEI1 protein, indicates that the p34SEI1 protein antagonizes the function of p16INK4a, which inhibits the cyclin-dependent kinases CDK4 and CDK6. See Sugimoto *et al.*, GENES & DEVELOPMENT 13:3027-3033 (1999). Sugimoto *et al.*, on pages 3031-32, explains that as a modulator of CDK4 kinase activity, p34SEI1 can “contribute to the deregulated growth of tumor cells.” Along these lines, page 27 of the instant specification states that “expression of CECRP is closely associated with cell proliferation.”

Hsu, *et al.*, THE EMBO JOURNAL, Vol. 20, No. 9, pp. 2273-2285 (2001), another post-filing date article, reports that TRIP-Br1 is a transcriptional regulator that stimulates E2F-1/DP-1 transcriptional activity. See Hsu, *et al.*, THE EMBO JOURNAL, Vol. 20, No. 9, pp. 2273-2285 (2001). Hsu, *et al.*, on pages 2282-83, explains that TRIP-Br1 is identical to the cyclin-dependent kinase 4 (cdk4) binding protein p34SEI1, and the BLAST results show that TRIP-Br1 and p34SEI1 are identical to the protein of the instant invention represented by SEQ ID NO: 3.

Accordingly, the claimed proteins and nucleotides of the instant invention do have a determined function with biological significance. Specifically, the claimed protein is related to cell proliferation and CDK4 kinase modulation, as well as transcriptional regulation. Additionally, the claimed protein and nucleotides may be used as a reagent for the diagnosis of a disease involving changes in levels of cyclin-dependent kinases CDK4 and CDK6, or to diagnose a disease implicated by changes in E2F transcriptional activity. Such diseases are disclosed in the specification at page 40. Because the claimed invention has at least one substantial and credible utility, the § 101 rejection is improper and should be withdrawn.

4. Claim Rejections – 35 U.S.C. § 112, First Paragraph

Claims 44-51, 54, and 58-59 are rejected under 35 U.S.C. § 112, first paragraph. Applicants respectfully request reconsideration and withdrawal of the rejection.

The Examiner reasons that because the claimed invention is not supported by either a substantially asserted utility or a well established utility, one skilled in the art clearly would not know how to use the claimed invention. Applicants have established a substantial and well-established utility as described above. The § 112, first paragraph, rejection is improper and should be withdrawn.

Further, the Examiner has rejected claims 44-51, 54, and 58-59 because the instant specification fails to adequately describe and enable proteins that are at least 90% identical to the polypeptide of SEQ ID NO: 3. Applicants do not agree with the Examiner. However, to expedite prosecution, Applicants have amended claims 44 and 51 to avoid this issue. Support for the amendment to claim 44 may be found in the specification at page 16, line 31 – page 17, line 2. Support for the amendment to claim 51 may be found in the specification at page 17, lines 8-15. The present version of the claims avoids this issue. The rejection should be withdrawn.

5. Claim Rejections – 35 U.S.C. § 112, Second Paragraph

Claims 44-51, 54, and 58-59 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Applicants respectfully request reconsideration and withdrawal of the rejection.

The Examiner states that it is unclear what cell cycle regulating activity the claimed protein has. As described above, Applicants have established an actual effect that the claimed protein has on the cell cycle from which one can determine the “metes and bounds of the term ‘cell cycle regulating activity.’” See Office Action at 8. Specifically, Applicants have demonstrated that the claimed protein is associated with unregulated growth of tumor cells, i.e., unregulated cellular proliferation. See Specification page 27, lines 17-18 and Sugimoto

*et al.*, pages 3031-32. Therefore, the § 112, second paragraph, rejection is improper and should be withdrawn.

6. New Claims

Applicants have added new independent claims 61 and 62 to more particularly point out the invention and distinctly claim the subject matter which applicant regards as the invention. New claims 61 and 62 recite a new limitation that the claimed proteins regulate cell proliferation. Support for new claims 61 and 62 may be found at page 27, lines 17-18 of the specification.

Conclusion

Applicants believe that the present application is in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

The Commissioner is hereby authorized to charge any additional fees which may be required regarding this application under 37 C.F.R. §§ 1.16-1.17, or credit any overpayment, to Deposit Account No. 19-0741. Should no proper payment be enclosed herewith, as by a check being in the wrong amount, unsigned, post-dated, otherwise improper or informal or

even entirely missing, the Commissioner is authorized to charge the unpaid amount to Deposit Account No. 19-0741. If any extensions of time are needed for timely acceptance of papers submitted herewith, Applicants hereby petition for such extension under 37 C.F.R. §1.136 and authorizes payment of any such extensions fees to Deposit Account No. 19-0741.

Respectfully submitted,

Date 6/18/04

By Eve L. Frank

FOLEY & LARDNER LLP  
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Eve L. Frank  
Attorney for Applicant  
Registration No. 46,785

Enclosure: Results of BLAST Search

USSN: 09/701,675

**BLAST2 Search Results**
[Sequences](#)    [Help](#)
[Retrieval](#)    [BLAST2](#)    [FASTA](#)    [ClustalW](#)    [CCG Assembly](#)    [Phrap](#)    [Translation](#)
[BLAST2 Manual](#)

Confidential - Property of Incyte Corporation SeqServer Version 4.6 Jan 2002

Program: blastp

Sequence ID(s):

 236062CD1 vs. genpept137

NCBI-BLASTP 2.0.10 [Aug-26-1999]



Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 236062CD1  
(236 letters)

Database: genpept137  
1,534,369 sequences; 474,463,515 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
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<input checked="" type="checkbox"/> <u>g21914610</u> SCDK4-binding protein p34SEI1 [Homo sapiens]	475	e-133
<input checked="" type="checkbox"/> <u>g14029834</u> TRIP-Br1 [Homo sapiens]	475	e-133
<input checked="" type="checkbox"/> <u>g12803669</u> CDK4-binding protein p34SEI1 [Homo sapiens]	474	e-132
<input checked="" type="checkbox"/> <u>g6746617</u> p34SEI-1 [Mus musculus]	411	e-113
<input checked="" type="checkbox"/> <u>g16359222</u> p34SEI-1 [Mus musculus]	411	e-113
<input checked="" type="checkbox"/> <u>g14029832</u> TRIP-Br1 [Mus musculus]	411	e-113
<input checked="" type="checkbox"/> <u>g12835034</u> unnamed protein product [Mus musculus]	411	e-113
<input checked="" type="checkbox"/> <u>g12842405</u> unnamed protein product [Mus musculus]	406	e-112
<input checked="" type="checkbox"/> <u>g14029830</u> TRIP-Br1 [Mus musculus]	381	e-104

>g6434876 CDK4-binding protein p34SEI1 [Homo sapiens]  
Length = 236

Score = 475 bits (1210), Expect = e-133  
Identities = 236/236 (100%), Positives = 236/236 (100%)

Query: 1 MLSKGKLRKREEEEKEPLAVDSWWLDPGHAAVAQAPPAVASSSLFDLSVLKLHHSLQQS 60

Exhibit 1

MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS  
Sbjct: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60

EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE 120  
Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE

EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE 120  
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE

DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS  
Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR  
Sbjct: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236

>g21914610 SCDK4-binding protein p34SEII [Homo sapiens]  
Length = 236

Score = 475 bits (1210), Expect = e-133  
Identities = 236/236 (100%), Positives = 236/236 (100%)

Query: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60  
MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS  
Sbjct: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60

EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE 120  
Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE

EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE 120  
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE

DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS  
Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR  
Sbjct: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236

>g14029834 TRIP-Br1 [Homo sapiens]  
Length = 236

Score = 475 bits (1210), Expect = e-133  
Identities = 236/236 (100%), Positives = 236/236 (100%)

Query: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60  
MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS  
Sbjct: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60

EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE 120  
Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE

EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE 120  
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVSPSPAAPSVDNLLASSDAALSASMASLLE

DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS  
Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR  
Sbjct: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236

>g12803669 CDK4-binding protein p34SEII [Homo sapiens]  
Length = 236

Score = 474 bits (1206), Expect = e-132  
 Identities = 235/236 (99%), Positives = 235/236 (99%)

Query: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60  
 MLSKGLKRKREEEEKEPLAVDSWWLDPGH AVAQAPPNAVASSSLFDLSVLKLHHSLQQS  
 Sbjct: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHTAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60

Query: 61 EPDLRHLVVNTLRRIQASMAPAAALPPVSPPAAPSVADNLASSDAALSASMASLLE 120  
 EPDLRHLVVNTLRRIQASMAPAAALPPVSPPAAPSVADNLASSDAALSASMASLLE  
 Sbjct: 61 EPDLRHLVVNTLRRIQASMAPAAALPPVSPPAAPSVADNLASSDAALSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
 DLSHIEGLSQAPQPLADEGPPRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS  
 Sbjct: 121 DLSHIEGLSQAPQPLADEGPPRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNEWLWAPASEGLKPGPEDGPKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
 MYDNEWLWAPASEGLKPGPEDGPKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR  
 Sbjct: 181 MYDNEWLWAPASEGLKPGPEDGPKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236

>g6746617 p34SEI-1 [Mus musculus]  
 Length = 236

Score = 411 bits (1044), Expect = e-113  
 Identities = 204/236 (86%), Positives = 214/236 (90%)

Query: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60  
 MLSKGLKRKREEEE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHSL+QS  
 Sbjct: 1 MLSKGLKRKREEEEETMEALSVDSCWLDPSPHAVAQTPTVASSSLFDLSVVKLHHSLRQS 60

Query: 61 EPDLRHLVVNTLRRIQASMAPAAALPPVSPPAAPSVADNLASSDAALSASMASLLE 120  
 EPDLRHLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE  
 Sbjct: 61 EPDLRHLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVDSSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
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 Sbjct: 121 DLNHIEDLNQAPQPQAEGPPRSIGGISPNGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNEWLWAPASEGLKPGPEDGPKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
 MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMMDVLVGTQALERPPGPGR  
 Sbjct: 181 MYDSELWLPASEGLKPGPENGPAKEEPPELDEAELDYLMMDVLVGTQALERPPGPGR 236

>g16359222 p34SEI-1 [Mus musculus]  
 Length = 236

Score = 411 bits (1044), Expect = e-113  
 Identities = 204/236 (86%), Positives = 214/236 (90%)

Query: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60  
 MLSKGLKRKREEEE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHSL+QS  
 Sbjct: 1 MLSKGLKRKREEEEETMEALSVDSCWLDPSPHAVAQTPTVASSSLFDLSVVKLHHSLRQS 60

Query: 61 EPDLRHLVVNTLRRIQASMAPAAALPPVSPPAAPSVADNLASSDAALSASMASLLE 120  
 EPDLRHLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE  
 Sbjct: 61 EPDLRHLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVDSSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
 DL+HIE L+QAPQP ADEGPPRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS  
 Sbjct: 121 DLNHIEDLNQAPQPQAEGPPRSIGGISPNGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNEWLWAPASEGLKPGPEDGPKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
 MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMMDVLVGTQALERPPGPGR  
 Sbjct: 181 MYDSELWLPASEGLKPGPENGPAKEEPPELDEAELDYLMMDVLVGTQALERPPGPGR 236

>g14029832 TRIP-Br1 [Mus musculus]  
Length = 236

Score = 411 bits (1044), Expect = e-113  
Identities = 204/236 (86%), Positives = 214/236 (90%)

Query: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60  
MLSKGLKRKREEEE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHSL+QS  
Sbjct: 1 MLSKGLKRKREEEEETMEALSVVDSCWLDPSPHPAVAQTPTVASSSLFDLSVVKLHHSLRQS 60

Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVDNLLASSDAALSASMASLLE 120  
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Sbjct: 61 EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPPAPSVDSSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS  
Sbjct: 121 DLNHIEDLNQAPQPQAEGPPGRSIGGISPNLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNEWLWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMMDVLVGTQALERPPGPGR  
Sbjct: 181 MYDSELWLPASEGLKPGPENGPAKEEPPELDEAELDYLMMDVLVGTQALERPPGPGR 236

>g12835034 unnamed protein product [Mus musculus]  
Length = 236

Score = 411 bits (1044), Expect = e-113  
Identities = 204/236 (86%), Positives = 214/236 (90%)

Query: 1 MLSKGLKRKREEEEKEPLAVDSWWLDPGHAAVAQAPPNAVASSSLFDLSVLKLHHSLQQS 60  
MLSKGLKRKREEEE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHSL+QS  
Sbjct: 1 MLSKGLKRKREEEEETMEALSVVDSCWLDPSPHPAVAQTPTVASSSLFDLSVVKLHHSLRQS 60

Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVDNLLASSDAALSASMASLLE 120  
EPDLRHLVLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE  
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPPAPSVDSSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS  
Sbjct: 121 DLNHIEDLNQAPQPQAEGPPGRSIGGISPNLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNEWLWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMMDVLVGTQALERPPGPGR  
Sbjct: 181 MYDSELWLPASEGLKPGPENGPAKEEPPELDEAELDYLMMDVLVGTQALERPPGPGR 236

>g12842405 unnamed protein product [Mus musculus]  
Length = 236

Score = 406 bits (1032), Expect = e-112  
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MLSKGLKR EEEE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHSL+QS  
Sbjct: 1 MLSKGLKRNGEEEETMEALSVVDSCWLDPSPHPAVAQTPTVASSSLFDLSVVKLHHSLRQS 60

Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVDNLLASSDAALSASMASLLE 120  
EPDLRHLVLVVNTLRRIQASM PA LPP P P APSVAD+LLASSDA LSASMASLLE  
Sbjct: 61 EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPPAPSVDSSLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLLGPATGCLLDDGLEGLFEDIDTS 180  
DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLLGPATGCLLDDGLEGLFEDIDTS  
Sbjct: 121 DLNHIEDLNQAPQPQAEGPPGRSIGGISPNLGALDLLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMMDVLVGTQALERPPGPGR 236  
 MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMMDVLVGTQALERPPGPGR  
 Sbjct: 181 MYDSELWLPASEGLKPGPENGPAKEEPPLEAELDYLMMDVLVGTQALERPPGPGR 236

>g14029830 TRIP-Br1 [Mus musculus]  
 Length = 223

Score = 381 bits (968), Expect = e-104  
 Identities = 190/223 (85%), Positives = 201/223 (89%)

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 MLSKGLKRKRE+EE E L+VDS WLDP H AVAQ PP VASSSLFDLSV+KLHHSL+QS  
 Sbjct: 1 MLSKGLKRKREKEETMEALSVDSCWLDPSPHPAVAQTPTVASSSLFDLSVVKLHHSLRQS 60

Query: 61 EPDLRHLVLVVNTLRRIQASMAPAAALPPVPSPPAAPSVDANLLASSDAALSASMASLLE 120  
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 Sbjct: 61 EPDLRHLVLVVNTLRRIQASMEPAPVLPPEPIQPPAPSVDALLASSDAGLSASMASLLE 120

Query: 121 DLSHIEGLSQAPQPLADEGPPGRSIGGAAPSLGALDLGPATGCLLDDGLEGLFEDIDTS 180  
 DL+HIE L+QAPQP ADEGPPGRSIGG +P+LGALDLGPATGCLLDDGLEGLFEDIDTS  
 Sbjct: 121 DLNHIEDLNQAPQPQADEGPPGRSIGGISPNLGALDLGPATGCLLDDGLEGLFEDIDTS 180

Query: 181 MYDNELWAPASEGLKPGPEDGPGKEEAPELDEAELDYLMDV LV 223  
 MYD+ELW PASEGLKPGPE+GP KEE PELDEAELDYLMDV LV  
 Sbjct: 181 MYDSELWLPASEGLKPGPENGPAKEEPPLEAELDYLMDV LV 223

Database: genpept137  
 Posted date: Sep 11, 2003 11:22 AM  
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 Number of sequences in database: 1,534,369

Lambda K H  
 0.310 0.132 0.383

Gapped  
 Lambda K H  
 0.270 0.0470 0.230

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 250279773  
 Number of Sequences: 1534369  
 Number of extensions: 11255951  
 Number of successful extensions: 47209  
 Number of sequences better than 10.0: 220  
 Number of HSP's better than 10.0 without gapping: 34  
 Number of HSP's successfully gapped in prelim test: 192  
 Number of HSP's that attempted gapping in prelim test: 46850  
 Number of HSP's gapped (non-prelim): 418  
 length of query: 236  
 length of database: 474,463,515  
 effective HSP length: 59  
 effective length of query: 177  
 effective length of database: 383,935,744  
 effective search space: 67956626688  
 effective search space used: 67956626688  
 T: 11  
 A: 40  
 X1: 16 ( 7.2 bits)  
 X2: 38 (14.8 bits)  
 X3: 64 (24.9 bits)  
 S1: 42 (21.7 bits)





Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Books
<input checked="" type="checkbox"/> Search Protein <input checked="" type="checkbox"/> for <input type="text"/> <input type="checkbox"/> Limits <input type="checkbox"/> Preview/Index <input type="checkbox"/> History <input type="checkbox"/> Clipboard <input type="checkbox"/> Details				<input type="checkbox"/> Go <input type="checkbox"/> Clear				
<input type="checkbox"/> Display default <input checked="" type="checkbox"/> Show 20 <input type="checkbox"/> Send to File		<input type="checkbox"/> Get Subsequence <input type="checkbox"/> Re						

1: AAK52831. TRIP-Br1 [Homo sa...[gi:14029834]

BLink, Domains, Links

**LOCUS** AAK52831 236 aa linear PRI 13-MAY-2001  
**DEFINITION** TRIP-Br1 [Homo sapiens].  
**ACCESSION** AAK52831  
**VERSION** AAK52831.1 GI:14029834  
**DBSOURCE** locus AF366402 accession AF366402.1  
**KEYWORDS**  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (residues 1 to 236)  
**AUTHORS** Hsu,S.I., Yang,C.M., Sim,K.G., Hentschel,D.M., O'Leary,E. and Bonventre,J.V.  
**TITLE** TRIP-Br: a novel family of PHD zinc finger- and bromodomain-interacting proteins that regulate the transcriptional activity of E2F-1/DP-1  
**JOURNAL** EMBO J. 20 (9), 2273-2285 (2001)  
**MEDLINE** 21231173  
**PUBMED** 11331592  
**REFERENCE** 2 (residues 1 to 236)  
**AUTHORS** Hsu,S.I. and Bonventre,J.V.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (29-MAR-2001) Dept. of Medicine, National University Hospital, 5 Lower Kent Ridge Road 119074, Singapore  
**COMMENT** Method: conceptual translation.  
**FEATURES**  
**source** Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/function="a CDK4-binding protein that renders the activity of cyclin D/CDK4 resistant to the inhibitory effects of p16(INK4a)"  
/name="hTRIP-Br1; transcriptional regulator interacting with the PHD-bromodomain"  
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121 dlshieglsq apqpladegp pgrrsiggaap slgaldd1gp atgccllddgl eglfedidts  
181 mydnelwapa seg1kpgped gpgkeeapel deaeldy1md vlvgtqaler ppgpgr  
//